



results of BLAST

# BLASTN 2.2.7 [Jan-02-2004]

RID: 1073687688-1793-130864213466.BLASTQ4

**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)  
2,018,459 sequences; 9,721,858,998 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

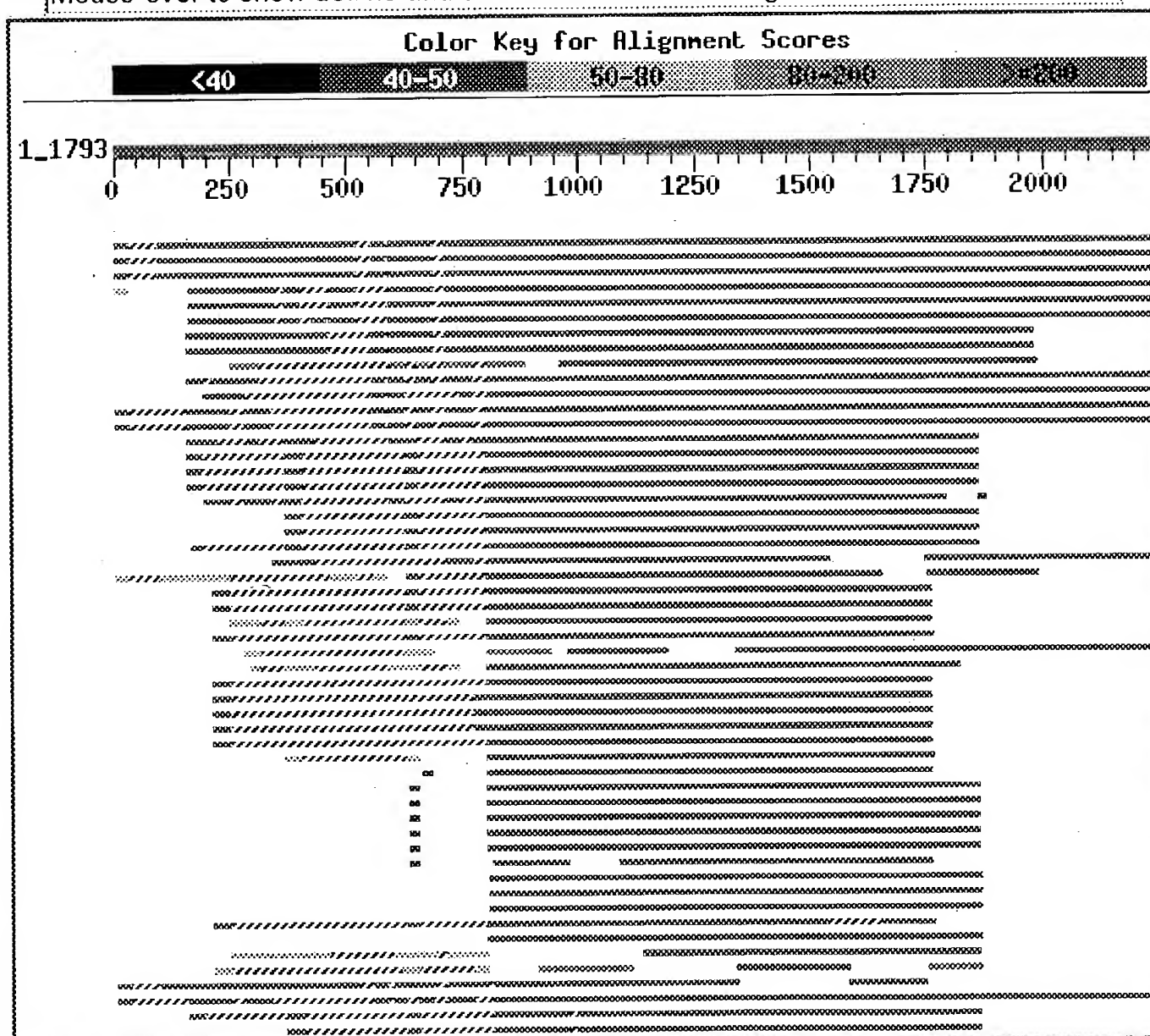
[Taxonomy reports](#)

Query=

(2237 letters)





































## Distribution of 459 Blast Hits on the Query Sequence





















Mouse-over to show define and scores. Click to show alignments








Sequences producing significant alignments:

Score E  
(bits) Value

<a href="#">gi 4996893 gb AF065164.2 AF065164</a>	Homo sapiens hyperpolariz...	<a href="#">2636</a>	0.0		98
<a href="#">gi 4775348 emb AJ012582.1 HSA012582</a>	Homo sapiens mRNA for h...	<a href="#">2630</a>	0.0		
<a href="#">gi 21359847 ref NM_001194.2 </a>	Homo sapiens hyperpolarization...	<a href="#">2630</a>	0.0		
<a href="#">gi 27476161 gb AC021413.16 </a>	Homo sapiens chromosome 15, clo...	<a href="#">2296</a>	0.0		
<a href="#">gi 28913160 gb AC139426.2 </a>	Homo sapiens chromosome 15, clon...	<a href="#">2279</a>	0.0		
<a href="#">gi 27901866 gb AC135731.6 </a>	Homo sapiens chromosome 15, clon...	<a href="#">2279</a>	0.0		
<a href="#">gi 24464597 gb BC039619.1 </a>	Homo sapiens hyperpolarization a...	<a href="#">2128</a>	0.0		
<a href="#">gi 3168875 gb AF064877.1 AF064877</a>	Homo sapiens ion channel ...	<a href="#">2094</a>	0.0		
<a href="#">gi 4206063 gb AF064851.1 AF064851</a>	Homo sapiens map 19p13.3;...	<a href="#">1860</a>	0.0		
<a href="#">gi 34862344 ref XM_343170.1 </a>	Rattus norvegicus hyperpolariz...	<a href="#">1669</a>	0.0		
<a href="#">gi 7407646 gb AF247451.1 </a>	Rattus norvegicus hyperpolarizati...	<a href="#">1661</a>	0.0		
<a href="#">gi 3242239 emb AJ225122.1 MMJ225122</a>	Mus musculus mRNA for h...	<a href="#">1542</a>	0.0		
<a href="#">gi 6680188 ref NM_008226.1 </a>	Mus musculus hyperpolarization-...	<a href="#">1542</a>	0.0		
<a href="#">gi 5708066 dbj AB022927.2 </a>	Oryctolagus cuniculus HAC4 mRNA ...	<a href="#">1391</a>	0.0		
<a href="#">gi 5734515 emb AJ238850.1 HSA238850</a>	Homo sapiens mRNA for h...	<a href="#">1308</a>	0.0		
<a href="#">gi 4775352 emb AJ132429.1 HSA132429</a>	Homo sapiens mRNA for h...	<a href="#">1308</a>	0.0		
<a href="#">gi 4885406 ref NM_005477.1 </a>	Homo sapiens hyperpolarization ...	<a href="#">1308</a>	0.0		
<a href="#">gi 3168867 gb AF064873.1 AF064873</a>	Mus musculus ion channel ...	<a href="#">1252</a>	0.0		
<a href="#">gi 7407650 gb AF247453.1 </a>	Rattus norvegicus hyperpolarizati...	<a href="#">1204</a>	0.0		
<a href="#">gi 25742570 ref NM_021658.1 </a>	Rattus norvegicus hyperpolariz...	<a href="#">1204</a>	0.0		
<a href="#">gi 38089857 ref XM_287905.2 </a>	Mus musculus similar to hyperp...	<a href="#">1181</a>	0.0		
<a href="#">gi 29169290 gb AY221752.1 </a>	Cavia porcellus hyperpolarizatio...	<a href="#">1065</a>	0.0		
<a href="#">gi 3168869 gb AF064874.1 AF064874</a>	Mus musculus ion channel ...	<a href="#">913</a>	0.0		
<a href="#">gi 28629107 gb AF488550.1 </a>	Homo sapiens hyperpolarization a...	<a href="#">851</a>	0.0		
<a href="#">gi 12652638 gb BC000066.1 BC000066</a>	Homo sapiens, clone IMAG...	<a href="#">847</a>	0.0		
<a href="#">gi 38327036 ref NM_020897.1 </a>	Homo sapiens hyperpolarization...	<a href="#">847</a>	0.0		
<a href="#">gi 7959336 dbj AB040968.1 </a>	Homo sapiens mRNA for KIAA1535 p...	<a href="#">845</a>	0.0		
<a href="#">gi 4775360 emb AJ133734.1 HSA133734</a>	Homo sapiens HCN2 gene,...	<a href="#">843</a>	0.0		
<a href="#">gi 2979528 gb AC004449.1 AC004449</a>	Homo sapiens chromosome 1...	<a href="#">843</a>	0.0		
<a href="#">gi 33312349 gb AF421883.1 </a>	Oncorhynchus mykiss hyperpolariz...	<a href="#">828</a>	0.0		
<a href="#">gi 26100858 dbj AK082719.1 </a>	Mus musculus 0 day neonate cere...	<a href="#">749</a>	0.0		
<a href="#">gi 26328056 dbj AK032225.1 </a>	Mus musculus adult male olfacto...	<a href="#">749</a>	0.0		
<a href="#">gi 7407648 gb AF247452.1 </a>	Rattus norvegicus hyperpolarizati...	<a href="#">749</a>	0.0		
<a href="#">gi 3242243 emb AJ225124.1 MMJ225124</a>	Mus musculus mRNA for h...	<a href="#">749</a>	0.0		
<a href="#">gi 6680190 ref NM_008227.1 </a>	Mus musculus hyperpolarization-...	<a href="#">749</a>	0.0		
<a href="#">gi 24657642 gb BC039156.1 </a>	Mus musculus, Similar to hyperpo...	<a href="#">749</a>	0.0		
<a href="#">gi 16758501 ref NM_053685.1 </a>	Rattus norvegicus hyperpolariz...	<a href="#">749</a>	0.0		
<a href="#">gi 6754167 ref NM_010408.1 </a>	Mus musculus hyperpolarization-...	<a href="#">702</a>	0.0		
<a href="#">gi 3242241 emb AJ225123.1 MMJ225123</a>	Mus musculus mRNA for h...	<a href="#">702</a>	0.0		
<a href="#">gi 2708315 gb AF028737.1 AF028737</a>	Mus musculus brain cyclic...	<a href="#">702</a>	0.0		
<a href="#">gi 7407644 gb AF247450.1 </a>	Rattus norvegicus hyperpolarizati...	<a href="#">662</a>	0.0		
<a href="#">gi 16758107 ref NM_053375.1 </a>	Rattus norvegicus hyperpolariz...	<a href="#">662</a>	0.0		

gi 20380241 gb BC028024.1	Homo sapiens hyperpolarization a...	616	e-173	
gi 3168873 gb AF064876.1 AF064876	Homo sapiens ion channel ...	519	e-144	
gi 28629105 gb AF488549.1	Homo sapiens hyperpolarization a...	502	e-138	
gi 32698745 ref NM_021072.1	Homo sapiens hyperpolarization...	502	e-138	
gi 16550669 dbj AK055840.1	Homo sapiens cDNA FLJ31278 fis,...	500	e-138	
gi 13346928 gb AF168122.2 AF168122	Oryctolagus cuniculus uO...	479	e-131	
gi 4775358 emb AJ133732.1 HSA133732	Homo sapiens HCN2 gene,...	469	e-128	
gi 12852741 dbj AK014722.1	Mus musculus 0 day neonate head...	469	e-128	
gi 4775356 emb AJ133730.1 HSA133730	Homo sapiens HCN2 gene,...	409	e-110	
gi 12025616 gb AC005559.2 AC005559	Homo sapiens chromosome ...	409	e-110	
gi 24431920 gb AC124407.4	Mus musculus BAC clone RP24-389C...	342	2e-90	
gi 16905311 gb AC009660.15	Homo sapiens chromosome 15, clo...	322	1e-84	
gi 18449993 gb AC068397.6	Homo sapiens chromosome 15, clon...	322	1e-84	
gi 4775359 emb AJ133733.1 HSA133733	Homo sapiens HCN2 gene,...	317	7e-83	
gi 4775355 emb AJ133729.1 HSA133729	Homo sapiens HCN2 gene,...	301	3e-78	
gi 38229393 gb AC110530.10	Mus musculus chromosome 9, clon...	297	5e-77	
gi 4775357 emb AJ133731.1 HSA133731	Homo sapiens HCN2 gene,...	290	1e-74	
gi 15870547 emb AJ326153.1 HSA326153	Homo sapiens genomic s...	276	1e-70	
gi 37693438 emb BX119923.12	Zebrafish DNA sequence from cl...	228	4e-56	
gi 37718626 emb BX284682.7	Zebrafish DNA sequence from clo...	214	5e-52	
gi 30722340 emb AL713999.28	Human DNA sequence from clone ...	201	5e-48	
gi 33355924 gb AY280847.1	Panulirus argus hyperpolarizatio...	191	4e-45	
gi 15875185 emb AJ330767.1 HSA330767	Homo sapiens genomic s...	155	5e-34	
gi 3970749 emb AJ012664.1 HVI012664	Heliothis virescens mRN...	141	5e-30	
gi 3168871 gb AF064875.1 AF064875	Mus musculus ion channel ...	131	4e-27	
gi 28570310 gb AC138520.2	Homo sapiens chromosome 5 clone ...	131	4e-27	
gi 6015988 gb AF155163.1 AF155163	Rattus norvegicus hyperpo...	118	5e-23	
gi 25012386 gb BT001547.1	Drosophila melanogaster RE10840 ...	110	1e-20	
gi 30039173 gb AY253222.1	Cavia porcellus hyperpolarizatio...	104	6e-19	
gi 21956546 gb AC117529.2	Homo sapiens chromosome 5 clone ...	102	2e-18	
gi 6015990 gb AF155164.1 AF155164	Rattus norvegicus hyperpo...	101	8e-18	
gi 23266274 gb AC126777.2	Homo sapiens chromosome 5 clone ...	89	3e-14	
gi 17402770 gb AC099514.2	Homo sapiens chromosome 5 clone ...	89	3e-14	
gi 31198194 ref XM_308045.1	Anopheles gambiae ENSANGP00000...	78	8e-11	
gi 30039171 gb AY253221.1	Cavia porcellus hyperpolarizatio...	72	4e-09	
gi 4803849 emb AJ133727.1 HSA133727	Homo sapiens HCN2 gene,...	70	2e-08	
gi 6015992 gb AF155165.1 AF155165	Rattus norvegicus hyperpo...	70	2e-08	
gi 4775354 emb AJ133728.1 HSA133728	Homo sapiens HCN2 gene,...	66	2e-07	
gi 6015998 gb AF155168.1 AF155168	Oryctolagus cuniculus hyp...	59	5e-05	
gi 33355926 gb AY280848.1	Apis mellifera hyperpolarization...	57	2e-04	
gi 27977186 gb AY192562.1	Cavia porcellus hyperpolarizatio...	57	2e-04	
gi 6016002 gb AF155170.1 AF155170	Oryctolagus cuniculus hyp...	57	2e-04	
gi 6015994 gb AF155166.1 AF155166	Rattus norvegicus hyperpo...	57	2e-04	
gi 12003345 gb AF211837.1 AF211837	Mus musculus hyperpolari...	55	7e-04	
gi 6016000 gb AF155169.1 AF155169	Oryctolagus cuniculus hyp...	51	0.011	
gi 38198225 dbj AP004770.2	Oryza sativa (japonica cultivar...	43	2.2	
gi 546583 gb S69800.1 S69800	OTK4=peptidyl-prolyl cis-trans...	43	2.2	
gi 546581 gb S69815.1 S69815	OTK4=peptidyl-prolyl cis-trans...	43	2.2	
gi 13677163 gb AC008073.4	Homo sapiens BAC clone RP11-507M...	41	8.4	
gi 12963276 gb AF322070.1 AF322070	Homo sapiens FK506-bindin...	41	8.4	
gi 965467 gb L37086.1 HUMFK506B	Homo sapiens FK-506 binding...	41	8.4	
gi 33639324 emb BX569695.1	Synechococcus sp. WH8102 comple...	41	8.4	
gi 30983667 gb AY223816.1	Homo sapiens Cohen syndrome 1 pr...	41	8.4	


<a href="#">gi 30983665 gb AY223815.1 </a>	Homō sapiens Cohen syndrome 1 pr...	<a href="#">41</a>	8.4	
<a href="#">gi 30983663 gb AY223814.1 </a>	Homo sapiens Cohen syndrome 1 pr...	<a href="#">41</a>	8.4	
<a href="#">gi 35493712 ref NM_017890.3 </a>	Homo sapiens Cohen syndrome 1 ...	<a href="#">41</a>	8.4	
<a href="#">gi 35493700 ref NM_152564.3 </a>	Homo sapiens Cohen syndrome 1 ...	<a href="#">41</a>	8.4	
<a href="#">gi 35493718 ref NM_184042.1 </a>	Homo sapiens Cohen syndrome 1 ...	<a href="#">41</a>	8.4	

## Alignments

Get selected sequences

Select all

Deselect all

☒ [gi|4996893|gb|AF065164.2|AF065164](#)  Homo sapiens hyperpolarization-activated, channel 2 (HCN2) mRNA, complete cds  
Length = 3372

Score = 2636 bits (1366), Expect = 0.0  
Identities = 1428/1449 (98%), Gaps = 19/1449 (1%)  
Strand = Plus / Plus

Query: 800 cagtgggaggagatcttccacatgacctatgacctggcca-cgcggtgatgaggatctgc 858  
|||||  
Sbjct: 1080 cagtgggaggagatcttccacatgacctatgacctggccagcgcggtgatgaggatctgc 1139

Query: 859 aatctcatcagcatgatgctgctgctctgccactgggacggctgcctgcagttcctggtg 918  
|||||  
Sbjct: 1140 aatctcatcagcatgatgctgctgctctgccactgggacggctgcctgcagttcctggtg 1199

Query: 919 cctatgctgcaggacttcccgcgcaactgctgggtgtccatcaatggcatggtgaaccac 978  
|||||  
Sbjct: 1200 cctatgctgcaggacttcccgcgcaactgctgggtgtccatcaatggcatggtgaaccac 1259

Query: 979 tcgtggagtgaactgtactccttcgcactcttcaaggccatgagccacatgctgtgcatc 1038  
|||||  
Sbjct: 1260 tcgtggagtgaactgtactccttcgcactcttcaaggccatgagccacatgctgtgcatc 1319

Query: 1039 gggtagggccggcaggcgcccgagagcatgacggacatctg-ctgacctatgctcagcatg 1097  
|||||  
Sbjct: 1320 gggtagggccggcaggcgcccgagagcatgacggacatctggctgacctatgctcagcatg 1379

Query: 1098 attgtgggtgccacctgctacgccatgttcacggccacgccactgccctcatccagtcg 1157  
|||||  
Sbjct: 1380 attgtgggtgccacctgctacgccatgttcacggccacgccactgccctcatccagtcg 1439

Query: 1158 ctggactcctcgcgggcgccagtaggagagaagtacaagcaggtggagcagtagcatgtcc 1217  
|||||  
Sbjct: 1440 ctggactcctcgcgggcgccagtaggagagaagtacaagcaggtggagcagtagcatgtcc 1499

Query: 1218 ttccacaagctgccagctgacttccgccagaagatccacgactactatgagcaccgttac 1277

1/9/04

Sbjct: 2220 a-----cgctgcagcaggcgggcgccatgagcttctgcccgcaggtggcgcgccgc 2271

Query: 1989 tcgtggggccgctggcgctcggctcgccgcgcctcgtgcgcgcgcccgccccggggcccg 2048

Sbjct: 2272 tcgtggggccgctggcgctcggctcgccgcgcctcgtgcgcgcgcccgccccggggcccg 2331

Query: 2049 cacctgccgcgcctcacccggggcccccgcccccgccagcccccgggcgcgcccgcca 2108

Sbjct: 2332 cacctgccgcgcctcacccggggcccccgcccccgccagcccccgggcgcgcccgcca 2391

Query: 2109 gccccggggcaccgcggacctcgccctacggcgggcctgccgcgcgcccgcccccttgctgggc 2168

Sbjct: 2392 gccccggggcaccgcggacctcgccctacggcgggcctgccgcgcgcccgcccccttgctgggc 2451

Query: 2169 ccgccctgccgcgcgcgcgcctgagccgcgcgctcgcgcccgactgtccgcctcgcagccct 2228

Sbjct: 2452 ccgccctgccgcgcgcgcgcctgagccgcgcgctcgcgcccgactgtccgcctcgcagccct 2511

Query: 2229 cgctgcctc 2237

Sbjct: 2512 cgctgcctc 2520

Score = 70.1 bits (36), Expect = 2e-08  
Identities = 36/36 (100%)  
Strand = Plus / Plus

Query: 156 ccaggccagcttcatgcagcgccagttcgggcgcgct 191

Sbjct: 509 ccaggccagcttcatgcagcgccagttcgggcgcgct 544

Score = 66.3 bits (34), Expect = 2e-07  
Identities = 34/34 (100%)  
Strand = Plus / Plus

Query: 278 agaccactgccccgtggatcgtgttcaacgtgg 311

Sbjct: 751 agaccactgccccgtggatcgtgttcaacgtgg 784

Score = 62.4 bits (32), Expect = 3e-06  
Identities = 32/32 (100%)  
Strand = Plus / Plus

Query: 366 catccccgtggactacatcttccttatcgtgg 397

Sbjct: 929 catccccgtggactacatcttccttatcgtgg 960

Score = 62.4 bits (32), Expect = 3e-06  
Identities = 34/35 (97%)  
Strand = Plus / Plus

Query: 308 tgggtgttgaacttccgcaccggcattgtgaccgag 342  
|||||  
Sbjct: 811 tgggtgttgaacttccgcaccggcattgtgatcgag 845

Score = 62.4 bits (32), Expect = 3e-06  
Identities = 32/32 (100%)  
Strand = Plus / Plus

Query: 651 gtggtctcggacaccttcttcctcatggacct 682  
|||||  
Sbjct: 780 gtggtctcggacaccttcttcctcatggacct 811

Score = 62.4 bits (32), Expect = 3e-06  
Identities = 34/35 (97%)  
Strand = Plus / Plus

Query: 461 cccgcgcgcggcgagcacggccaagggcagcccga 495  
|||||  
Sbjct: 296 cccgggcgcggcgagcacggccaagggcagcccga 330

Score = 60.5 bits (31), Expect = 1e-05  
Identities = 31/31 (100%)  
Strand = Plus / Plus

Query: 770 accaagatcctcagcctcctgcgggtgctgc 800  
|||||  
Sbjct: 1020 accaagatcctcagcctcctgcgggtgctgc 1050

Score = 60.5 bits (31), Expect = 1e-05  
Identities = 31/31 (100%)  
Strand = Plus / Plus

Query: 741 agaagggcattgactccgaggtctacaagac 771  
|||||  
Sbjct: 961 agaagggcattgactccgaggtctacaagac 991

Score = 60.5 bits (31), Expect = 1e-05  
Identities = 31/31 (100%)

Strand = Plus / Plus

Query: 592 acttcaggttctactgggacttcacccatgct 622  
 |||  
 Sbjct: 661 acttcaggttctactgggacttcacccatgct 691

Score = 60.5 bits (31), Expect = 1e-05  
 Identities = 31/31 (100%)  
 Strand = Plus / Plus

Query: 217 gcgggggcctggatcatccacccgtacagcg 247  
 |||  
 Sbjct: 630 gcgggggcctggatcatccacccgtacagcg 660

Score = 58.6 bits (30), Expect = 5e-05  
 Identities = 30/30 (100%)  
 Strand = Plus / Plus

Query: 428 gcctctcacgcctgatccgctacatccatc 457  
 |||  
 Sbjct: 1051 gcctctcacgcctgatccgctacatccatc 1080

Score = 58.6 bits (30), Expect = 5e-05  
 Identities = 30/30 (100%)  
 Strand = Plus / Plus

Query: 398 cggcacgcgccctgcgcatcgtgcgcttca 427  
 |||  
 Sbjct: 991 cggcacgcgccctgcgcatcgtgcgcttca 1020

Score = 58.6 bits (30), Expect = 5e-05  
 Identities = 30/30 (100%)  
 Strand = Plus / Plus

Query: 711 cgtggttcgtgggtgacttcgtgtcctcca 740  
 |||  
 Sbjct: 901 cgtggttcgtgggtgacttcgtgtcctcca 930

Score = 58.6 bits (30), Expect = 5e-05  
 Identities = 30/30 (100%)  
 Strand = Plus / Plus

Query: 338 ccgagaagatcaagaagaagtatctgcgca 367  
 |||



Sbjct: 871 ccgagaagatcaagaagaagtatctgcgca 900

Score = 58.6 bits (30), Expect = 5e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 622 tcccagtgggcatcaccttcttcaaggatg 651  
|||||  
Sbjct: 721 tcccagtgggcatcaccttcttcaaggatg 750

Score = 58.6 bits (30), Expect = 5e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 248 tgctgttcatgggtgggaaacctcatcatca 277  
|||||  
Sbjct: 691 tgctgttcatgggtgggaaacctcatcatca 720

Score = 58.6 bits (30), Expect = 5e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 188 cgctgcggatgttcggcagccagaaggccg 217  
|||||  
Sbjct: 571 cgctgcggatgttcggcagccagaaggccg 600

Score = 58.6 bits (30), Expect = 5e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 555 cgctcctgcagccgggcgtaacaagttct 584  
|||||  
Sbjct: 541 cgctcctgcagccgggcgtaacaagttct 570

Score = 58.6 bits (30), Expect = 5e-05  
Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 93 acagctcgtgcggccgccccggcaccgccg 122  
|||||  
Sbjct: 271 acagctcgtgcggccgccccggcaccgccg 300

Score = 58.6 bits (30), Expect = 5e-05

Identities = 30/30 (100%)  
Strand = Plus / Plus

Query: 1 cggctccgctccgcactgcccggcgccgcc 30  
|||||  
Sbjct: 1 cggctccgctccgcactgcccggcgccgcc 30

Score = 50.9 bits (26), Expect = 0.011  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 129 cccaaggtgtcgttctcgtgccgcgg 154  
|||||  
Sbjct: 396 cccaaggtgtcgttctcgtgccgcgg 421

Score = 47.0 bits (24), Expect = 0.15  
Identities = 24/24 (100%)  
Strand = Plus / Plus

Query: 496 gcagccccgcggggcccgagggcc 519  
|||||  
Sbjct: 361 gcagccccgcggggcccgagggcc 384

>gi|4775348|emb|AJ012582.1|HSA012582 Homo sapiens mRNA for hyperpolarization  
Length = 3459

Score = 2630 bits (1363), Expect = 0.0  
Identities = 1427/1449 (98%), Gaps = 19/1449 (1%)  
Strand = Plus / Plus

Query: 800 cagtgggaggagatcttccacatgacctatgacctggcca-cgcggtgatgaggatctgc 858  
|||||  
Sbjct: 1098 cagtgggaggagatcttccacatgacctatgacctggccagcgcggtgatgaggatctgc 1157

Query: 859 aatctcatcagcatgatgctgctgctctgccactgggacggctgcctgcagttcctgggtg 918  
|||||  
Sbjct: 1158 aatctcatcagcatgatgctgctgctctgccactgggacggctgcctgcagttcctgggtg 1217

Query: 919 cctatgctgcaggacttcccgcgcaactgctgggtgtccatcaatggcatggtgaaccac 978  
|||||  
Sbjct: 1218 cctatgctgcaggacttcccgcgcaactgctgggtgtccatcaatggcatggtgaaccac 1277

Query: 979 tcgtggagtgaactgtactccttcgcactcttcaaggccatgagccacatgctgtgcatc 1038  
|||||  
Sbjct: 1278 tcgtggagtgaactgtactccttcgcactcttcaaggccatgagccacatgctgtgcatc 1337